

SEQUENCE ANNEX 1a - Complete genomic sequence of EHV-1 strain V592

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SEQUENCE ANNEX 1b - EHV-1 strain V592 feature table

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CDS           complement(11116..12096)
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 repeat_region 45278..45367
 /note="insertion of 45bp compared with AB4: imperfect
 repeat of subsequent sequence - changed residues in
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 /gene="EHV-1 ORF25"
 CDS complement(46886..47245)
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 /function="located on tips of hexons"
 /note="homologous to HSV-1 UL35"
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 CDS complement(47337..48164)
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 /function="role in envelopment at nuclear membrane,
 probable interaction with pORF29"
 /note="homologous to HSV-1 UL34"
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 gene complement(48303..48725)
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 CDS 59177..61504
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 with pORF28"
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 RRLECTCDHITRQMAVRVANIDIARHLPHALSVASERRAAEAALRALEARRVQGHN
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 gene 61366..64308
 /gene="EHV-1 ORF33"
 CDS 61366..64308
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 /function="role in virus binding/entry"
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 CDS 64512..64994
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 /note="homologous to VZV gene 32"
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/translation="MDSPRGISTATGDAHAEAAVSPAAEIQIKTEAPDVGPEATTEC
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gene complement(65087..66076)
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gene complement(65087..67027)
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CDS complement(65087..66076)
/gene="EHV-1 ORF35.5"
/note="homologous to HSV-1 UL26.5"
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CDS complement(65087..67027)
/gene="EHV-1 ORF35"
/function="capsid maturation and scaffold activities"
/note="homologous to HSV-1 UL26"
/codon_start=1
/product="capsid protein"

/translation="MDAYTVDGNAVSLPIYVAGYIALYDMGDGGELTLTRETVAALP
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TPENAVAPFKRLSPSSREELLITAREAQSR LGDAATWHLSEDTLTRVLLSTAVNNMLL
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gene complement(67146..68909)
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CDS complement(67146..68909)
/gene="EHV-1 ORF36"
/function="role in DNA packaging"

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        /note="homologous to HSV-1 UL24"
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        gene        69843..70901
        /gene="EHV-1 ORF38"
        CDS        69843..70901
        /gene="EHV-1 ORF38"
        /note="homologous to HSV-1 UL23"
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        /product="thymidine kinase"

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gene      71125..73671
          /gene="EHV-1 ORF39"
CDS       71125..73671
          /gene="EHV-1 ORF39"
          /function="virus entry, interacts with gL"
          /note="homologous to HSV-1 UL22"
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gene 76726..77445
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CDS 76726..77445
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 with gK"
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gene 77636..81766
 /gene="EHV-1 ORF42"

CDS 77636..81766
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 /note="homologous to HSV-1 UL19"
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gene 82016..82960
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CDS 82016..82960
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gene complement(83081..88850)
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CDS complement(join(83081..84253,87819..88850))
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IVFASSHNTNGIRGQDFNLLFVDEANFIRPEAVQTIIGFLNQTNCKIIFVSSTNTGKA
STSFYLNKGAADDLLNVVITYICDEHMERVKAHTNATACSCYILNKPVFITMDGAMRN

TAEFLPDSFMQEIIIGGNVSGAHRDEPVFTKTAQDRFLLYRPSTVANQDIMSSDLYV
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 VFAIHKRPFDSVRVAVEGNSSQDAAVAIATNIQLELNTLRRADVPMPGAVLFYHCTP
 HGSSVAYPFFLLQKQKTGAFDHFIFKAFNSGSVLASQELVSNTVRLQTDPEYLLTQMK
 NLTEVVTGTSETRVFTGKRNGASDDMLVALVMAVYLSSLPPTSDAFSSLPAQ"
 gene 84413..86533
 /gene="EHV-1 ORF45"
 CDS 84413..86533
 /gene="EHV-1 ORF45"
 /note="homologous to HSV-1 UL17"
 /codon_start=1
 /product="putative product ORF45"
 /translation="MDAHIANETKHLVLVHGNSKTRALVHIIVPDACLKKAGVDPVKLS
 DRHRASPSAAPVFRVFAQTRYHATGECSLWRTVFAGYVPSGAIVSALVPTVPADHPRL
 FQSTPDSGGLFVSLEIECDADGRFDAFTLVALRVDIADDPRTTEVLFTYDELLPPGTR
 YGADSKRVALLCRQFVAYVNSHPTVSQSAVTAASHIEAAVAEDVKSASGPQVSYGARI
 DPAEYLFSGGGFDNHQALARLEDDDDKEIMSLIRRASEVIAKRNPVRVLSNPEVNGDAH
 RRQCVASGLRQGARGAHASDSHARVGFNSSIHDATAALLGLEPPDSGRFVNSSGPQRHL
 PPQGPRSPASRDCQSGMLDDVLLLTPENSNPLTPLDWLDVGHAAGVAGDTPRDVWRRR
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 NLPPETRGEIAKFPMLTVPLGDTPPPVAADFADAAELALIDHFRGACVSALLKAISER
 LRAEPRMSQLIEYDIPNNNRDCIISVAQRAPELLEAVALAIQNVTVTFCNSALMLSA
 LSHLNILSGNKRGRLPYHRSWLPFLAGGADAFLEFDYSSSGGEVVKVSPVPLAILVTAT
 RTGQHSCRFARGAPDSSSKTYERYLPGEYAYICVGLNRSFEALVVLPGGFACRASAA
 RKLAWPAHLVEPILERYCWTIPSH"
 gene 86553..87665
 /gene="EHV-1 ORF46"
 CDS 86553..87665
 /gene="EHV-1 ORF46"
 /note="homologous to HSV-1 UL16"
 /codon_start=1
 /product="tegument protein"
 /translation="MMAAASDCLSLWEGSASSPNRQLTPEAVNCLTEALTEDVAVLR
 LIRSDPRVKIFMAVSVLTPRLARFAPPPKLTHTAKCAVIMIYLTRPKALALQPKQFH
 MLVTFNKASVYSLVVRVKTKFPFVGTQRFRAVFQDPESIGLPSDIPDPAAENIPTVIN
 DRLDVSNFATPAQPPKDKYDCCVLAPGVWWSNANKAIYFLQMDVALLALCPAGWKARG
 LGIILGRLLNHQEGCATCRFTEHSDPLNATADSVATPESCLCWAPCLWRKAHQRELT
 EGDYRLFVFLFMDAVERVRLTGLRRSPKITANLADLVVGIGPHGQQIPVNNAGWKLVA
 LDADISRLIVCGCYALRYICPPTNSKHQPSSPDEYA"

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gene      88880..89833
          /gene="EHV-1 ORF48"
CDS       88880..89833
          /gene="EHV-1 ORF48"
          /note="homologous to HSV-1 UL14"
          /codon_start=1
          /product="probable tegument protein"

/translation="MSFSARSRRQRLQLEEAYQREMIFKMHTLDLVREGVKNRSPAFV
RAFTSAKEASLDLDRYMQAHSRVGRVEQNARALAQRVEAQAAGVGEILDRHRRFLHPDF
IDNFDSREDSIVEREERLGDVLSNDGCGGGGEVGDGPQEWLGHEDEALLMRWMLLEEAP
RVSTRIAADPHSPRSTCPAPRKAPEDARCARKPGEVNNYTPSAQPRSQETTVDHLAS
PDEGTRLGDRTRDLEHHSTAPMRTHPNVLASERRRLGVVHQREKSSSESQESATRSKAI
          VGQEDQKWLGGIPPLSDEELQVDMGIPTMNGPIYPDYHRTA"
gene      89302..91086
          /gene="EHV-1 ORF49"
CDS       89302..91086
          /gene="EHV-1 ORF49"
          /function="serine/threonine protein kinase"
          /note="homologous to HSV-1 UL13"
          /codon_start=1
          /product="tegument protein"

/translation="MARSRRRSSVDEMDVGGSATSEYENCGGPSFSPNLNLSRPKKSTR
GRSLRSAQAWGGKQLHPERSTPLARNDGPPSSKPRRRHEVGRSNKGLGASLDRTDED
SQCPRIRASAIRCGASTRKIVRITGECDAQQGDSRPGRSEMAGWHSPPKRRRTPSRHG
NSDNERSHLPRLSSHGVVRVGGRPPLTQTPLOKTIILQPKLVRKVFMPFTFTVNPEMHYR
RVALGEIPKFGGAGSYGEVQIFKQTGLAIKTASSRSCFEHELAVSLLTGECSLRAQAS
LGIGGIICLMAFSLPSKQMVFPAYDADLNAYGYRLSRSGPPSVLVTESIERAFIQLGR
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GEEEIKTLRLPRSASQMTFSFVIGHGLNQPISVIADFINNSGLAKSTGPIKHDVGLTI
DLYALGQALLELLLVCISPCLSVPILRATATYYYYSNKLSVDYALDLLAYRCSLYPAL
FPTTPLTTIYGIPWDQVEGVFESIAGAAHREAFRAHLERYRLTHRRLFASIRIPSAFT
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gene      91068..92765
          /gene="EHV-1 ORF50"
CDS       91068..92765
          /gene="EHV-1 ORF50"
          /note="homologous to HSV-1 UL12"
          /codon_start=1
          /product="deoxyribonuclease"

/translation="MDSSPVTYSGEPPYKLRRRLSPSYPYVSKLRERCASKIETLSEGS
ARDSLEEEDVSEAMATGAFLATRLYLPSVLPQRITTLTFLDHFKKSRPLPNSDKRLNP
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GLLMDARTGVVGASLDMLVCDRDPGVLSPHSTQTTLDDFFAIKCRACKYLFDPDLFSPV
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NRRCGDFDRDHIALNLDASSDVWLFSEPDLESETITPARWDTGELALSVPVFANPRHP
NFKQILVQAYVLSGHFPDHLRPFVTFIGRHRKRCEEKTFITICDRPEGSPYNLNEV
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  gene          92717..92941
                /gene="EHV-1 ORF51"
  CDS           92717..92941
                /gene="EHV-1 ORF51"
                /note="homologous to HSV-1 UL11"
                /codon_start=1
                /product="tegument protein"

/translation="MGQRLSCGCFRTDQLVTHSGEVVSLNADTFEEFSMEEFDIPPPP
              PLPKPVFKQPGPYKIPARSQRCPSKRRDPY"
  gene          complement(93053..94405)
                /gene="EHV-1 ORF52"
  CDS           complement(93053..94405)
                /gene="EHV-1 ORF52"
                /function="role in envelope fusion, interaction with gN"
                /note="homologous to HSV-1 UL10"
                /codon_start=1
                /product="envelope glycoprotein M (gM)"

/translation="MARRGA AVAE EPLL PSSGIVGIGPIEGINWRTWLVQVFCFALTT
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VAFLYYTTLVLVAISFYLIISAVLVRRYARGKECTAVAGCTRPTTTLIASHVTLVLGT
LATWLLQVVILLLSHKQAVLGAAYVVVHFVSLVFFCMSFSGLGTASAQYSSNLRILKT
NLPALHKMAGPGRAVMTNLGMGMLGISLPILSLMLGIILANSFHITLWQTVTVAVGVF
VALGLMFLIIVELIVSHYVHVLVGPALAVLVASSTLAVATHSYFVHFHAMVSVQAPNL
ATASKAIVGIMAVISIIMLVVRLVRAIMFHKRNTFEYGRVKTVSSKARRYVNKVRGP
RRNPQPLNVAESRGMLLAEDSETDAEPIYDVVSEEFETEEYDDPQRV PERSHREYR
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  gene          94323..96986
                /gene="EHV-1 ORF53"
  CDS           94323..96986
                /gene="EHV-1 ORF53"
                /function="helicase"
                /note="homologous to HSV-1 UL9"
                /codon_start=1
                /product="origin binding protein"

/translation="MPSIGPIPTIPDEGSRGSSATAAPRRAMASYRDTTLGGRAEGVA
FSAVEDSYTSSVSLARMLYGGDLEEWVRHTRPGVSLEIQSRAPVRFPPPNPSSRRVT

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VVRAPMGSGKTTALLKWLGEALDAPDISALVVSRRSFTRTLAKRFNDAELPGFATYF
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 VDALLTRLKTCPRVIAMDATANAQLVDFLASARGERSVHVIINSFAAPGFSQRDGT
 LRTLGTDLRAALGFVLVDDENGTKVMETDSRPISARLREVNSAGFFGRMLMDRLVAGR
 NVCVFSSTVSFSEIVARFCSQFTDSILVLNSLRPSEDVAFWGGVRVLIYTTVVTVGLS
 FDTAHFHSMFAYVKPMSHGPDMSVYQSLGRVRELIHNELLVYVDSSGARAEPIFTM
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 RGPGGIAATPTEVFENDDVAVFIQKYL RPGVAHDEILALLVELNSPIVREQFVNVAVL
 GACLRLPAALESPEVFAGVYKHYASGVVPVISDAGALESVSITPDVNVLARWDLYKSC
 TRHARDLAWDPSRGGSGLDMSDEFITNTLSADYNRFQSLLEIACNVTPLEMLAAGA
 VRGVTTALSGRPKSRVPLSKGEHAVSLFKVLWEDVFGAKLAKSTQTFPGGVRVKNLRK
 DEIVALLESVNVNHSECKTHRELYALLMCNRKLFAGPRYKLRAPKWSRNLCFLELDNT
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 gene 97002..99257
 /gene="EHV-1 ORF54"
 CDS 97002..99257
 /gene="EHV-1 ORF54"
 /note="homologous to HSV-1 UL8"
 /codon_start=1
 /product="component of DNA helicase-primase complex"
 /translation="MEGSVEWFNGHVCATSIYSLWTDPHHPGHLQALVYMLCRRGSDY
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 PRAAIVNVSV
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 FYRK
 YD
 SVQQPANKRRGDMADLFVVHERTLLLGGCKRMGVKVL
 LPTFDCLVASSQSVSGLAAM
 ALYKQWHATLFSVELPDTVVQIFAYLGP
 ELNPCGEEVDYCCFVGFPGLPTLKASSSTT
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 ESEAKRVEGAVHRLQLGTE
 DDWGAGRVSCILESDAVMQGPWFAKFDFSAFFPTLY
 LLLFPANERLAEVVRLRARGQH
 PTLKLALVSFFGGLQHINPVAYRSIIALSNGISK
 RLEHEVNQRGFAICTYVKDGF
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 FSLPEGVHLNLRLEGLFTDAI
 SWSTHCYWLYNRFTKMEDFVGFP
 AKSGAGRAAKASLSALLPLVA
 AAVCDSSDMSTLHQ
 S
 VRGACEQLVAGAF
 AERNNPQFWSTRTGIESSTLLPPAVYRNGSLLDRDCGQREIVL
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 KHDCE
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 SIFKTYLSMLNRAISASCD
 ADESMNVD
 FPISDYAFLFT"


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gene      complement(99352..100263)
          /gene="EHV-1 ORF55"
CDS       complement(99352..100263)
          /gene="EHV-1 ORF55"
          /note="homologous to HSV-1 UL7"
          /codon_start=1
          /product="putative product ORF55"

/translation="MSATMRAEIDPLAHSATVDEMVEAITKGDDSVTTIVDDLWHAT
PRFVTEVREVPGLPPSFTTTSVTDMRVDASSEKLMLTLDGQEGSEISCETYMRSCLDL
PAFKGFSLFVVTPLEDRVNVLGVAPVILSHRLVLYRPTDLIDFTLCIIQMYLENCSTK
RATSSLFVQIECILRNISKTTITPLLKMRRMLYIGATWTLNLTLMCVTNHNPFDQARVLP
NYMMAKMLLGQKSNTPAILDAIYSAGYRQTL SKRPITPCPSGVLRCNKAHLNAPLCTK
          VVADTLYSWWTATDEKPVPEIYVLYD"
gene      complement(100061..102322)
          /gene="EHV-1 ORF56"
CDS       complement(100061..102322)
          /gene="EHV-1 ORF56"
          /note="homologous to HSV-1 UL6"
          /codon_start=1
          /product="minor capsid protein"

/translation="MSADSIIEPKQKRLRYADANKGRKVERKNTPRFEATTGLQSPGEE
EQISADGGWVLIHPTPKTMLFKEILMGELGYTEGQGVYNAIRSTEAAIRQIQTTILT
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LLDFVRSITACFSASEPDGTASFAYIDWIACLGLIPLQRLKRAPGATVHPKLWRKLP
TDVPSLESCVDERDLAGKLYVANSLLREGLEAVVELARCTASVAIMDYDRVNIIFYHYT
RREVVAIDSTTGKRGECLVLWQPIWKDGSVLFDSPLQRICGEVCNCHALREHAKLCQL
LNTVPVKILVGRKKDEAQGPWASKAVDKLMGEGEELHSSSAASRLVKLIVNMKSMRH
IGDITETVRSYLNSTNLLSGAQVDTSLPGFGQSGKTKQGGNMPVQEAFRTSVINGI
NGMLEGYVNNLFKTIEDLRTGNSGLLDQLRDRESEITHLREQLLRVSQAAADGSTQPG
ASSAALPGSGAKSGAGGLGHEVIDIRNLMGDDGYVANSFQSRYPAYTADMERLSRLW
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SEEELCVAVFKKTRLEAYLTELTSTLFVARVRNSIAALNSTKRDLPVNDNEAQSDEEQ
LKPSDERYYEGRDRSASPQRDRGRNGRGYHKRRRFSNNYRRRSGLARDSSIRDRSQRG
          SRPTPLLHDHVG"
gene      102306..104951
          /gene="EHV-1 ORF57"
CDS       102306..104951
          /gene="EHV-1 ORF57"
          /function="helicase"
          /note="homologous to HSV-1 UL5"
          /codon_start=1
          /product="component of helicase-primase complex"

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/translation="MESADILPGSRGTVDRRCEGSEEKITPPRPVEDFNPQLFPNEVY
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ISGNAGSGKSTCIQTLNETMDCVITGATRVAQNVYTKLSSAFATRHINTIFQEFGR
GNHVQAQLGKYQYSCSSPPPIEELQKRDIVVYWEVLVDITRRLFESTASRGEFENIR
ALERLLGRAPGSLTRLAFCTNGSLPAFTRTNIVIIDEAGLLGRHLLTVVVYCWMLNA
AYKSPQYAEKGVPVIVCVGSPTQTDLESRFEHKNLKCHVRSSENVLTHIITNRTIRE
YVSLSTNWAIFINNKRCEYEFGELMKVLEYGLPITEEHMRLVDTFVVPEAYINNPAN
LPGWTRLYSSHKEVSAYMAKLHAHLKVSGERQFVVFVTLPAYTFVKTAADFDEYKKITQQ
PSLSLDKWLAAANASRVSNYSQSRDQDAGKTQCEYYSEHGTVVARTDVTYVLNSQVSVT
TRMRKFVFGFSGTFETFDVAVLKDDAFIKTQGETSVEYAYRFLSTLLFSGMINFYNFLK
RPGLDGRVREAYRRMAALTAKLIPGASVLESACDNPSGAPLNFRGLTDPPGFTGGTT
NDWDDNDNVFAALNEGAIDMLYCNYEFVRPETTQEVYSQFLMLKTMFVGRYSIFMDL
FGGDFESSPFDTFVDNISYKGCEIFVGS MRGGVSSIALQTD SYTLMGYTSAPVYPFVE
ELARRKLHEGIAELFGAMNMPRMVLRDQHGFM SVLNVNLSEFVESVDDVELDMATAVD
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RHERDTVISEHILAALRDRDVQIVY"

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gene      105001..105678
          /gene="EHV-1 ORF58"
CDS       105001..105678
          /gene="EHV-1 ORF58"
          /note="homologous to HSV-1 UL4"
          /codon_start=1
          /product="putative product of ORF58"

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/translation="METCSPPVTFITYALYGIKTSPAWTLPNFEQVICSCDWGYRLIA
VGAESKCDVTPQGSFVIQHGASITALVLDCGVEFCSYAFTHAENTRVPLTTEDGSVLV
VPFCGWVCVGRDRCLRSMGGVLTISWDTSQTAYISVAVYRPPTLQCHALDCTRAETT
VCSTAAITDASESDPLYADQEGDQTQDQDGGHDFLETILMESDLYGTNGASALLEPCF
PCLSNND"

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gene      complement(105808..106347)
          /gene="EHV-1 ORF59"
CDS       complement(105808..106347)
          /gene="EHV-1 ORF59"
          /note="positional homologue to VZV gene 57"
          /codon_start=1
          /product="putative product of ORF59"

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/translation="MDVFGRGRAATADDYRRFLERNRRAAKLAAATTPHTASSRQQ
PEVSARPRHRSLSRRNSVPHYDPHAGAGGDGQLALSERPSGTLGALAMAAQRRKSIG
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QTQPHQGRPRPRRNTLRHM"

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gene      complement(106409..107047)
          /gene="EHV-1 ORF60"
CDS       complement(106409..107047)
          /gene="EHV-1 ORF60"
          /note="homologous to HSV-1 UL3"
          /codon_start=1
          /product="putative product of ORF60"

/translation="MESALTVLSGWGPVEVVTGPVADHLTEMPPAPTGTCTTTST
PTPLCVPDLSVESIKGLAPDGENANYVGFDTMFMVSSIDELGRRQLTDTIRKDLRVTL
AKFTIACTKTSSFSSASSTRRRKRHCPSSSERVMRSNKSLOMFVLCRRRAHAKQIRDQLQ
SVIQARKPRKYYTRSSDGRTHPVVPVYIYEFSAVDKVYLHRDNVIEADAQAK"
gene      complement(107137..108075)
          /gene="EHV-1 ORF61"
CDS       complement(107137..108075)
          /gene="EHV-1 ORF61"
          /note="homologous to HSV-1 UL2"
          /codon_start=1
          /product="Uracil-DNA glycosylase"

/translation="MSSACDHETEASHVNIPETTPPEENGNSSTPTSEIGPACVVSPA
PGETGAPPPKRRRPCGLPQGVALINTSVSTHPLFTTSCQSSWEDVEREFNIAPSWRPI
LEREMQQPYVRLLLNEYKLRCASEEVFPPKEDIFAWTRFSPPEKVRVVIVGQDPYHAP
GQAHGLAFSVRKGVPPPSLRNIYSAVQKSYPSFRHPMHGFLERWAEQGVLLINTTLT
VARGKPGSHATLGWHRLVRAVIDRLCTTSQGLVFMLWGAHAQKSCSPNRQHHLVLTYG
HPSPLSRVNFRCDFHLEANAYLTKTGRKPDWQIE"
gene      complement(108078..108734)
          /gene="EHV-1 ORF62"
CDS       complement(108078..108734)
          /gene="EHV-1 ORF62"
          /function="role in virus entry, interaction with gL"
          /note="homologous to HSV-1 UL1"
          /codon_start=1
          /product="envelope glycoprotein H (gH)"

/translation="MYQILIGCVWQKSPYINQCTEFQPPLSFVTPERMRRFMRCWARL
ELVYMLAWIVTTKLVKATRLDFTWGPGEPPKRILEASCGSGPIMKGQLFTSPNIKLLN
RTTGIMVKAHCNPPEAILWVDTPPKPVWVNPFAVVQGLAEDVTNGNMPQDFKEKLLFA
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repeat_region 108895..108984
               /note="variable copy number in V592"
               /rpt_unit=GCTAGCGCTAACGCTAGG
gene          complement(110353..111951)
               /gene="EHV-1 ORF63"
CDS           complement(110353..111951)
               /gene="EHV-1 ORF63"
               /note="homologous to HSV-1 RL2"
               /codon_start=1
               /product="transcriptional regulator"

/translation="MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCP

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 EEELTRQFWPMFHEDTVPFVTDLIVQAEKCVASRPILPIARGRGVEYIDSSSSSSSSSE
 EETDSDIEVDPNNLTDPEDTSDDETSTDNSSAQAPRQEDSRPARARPGPPTRGRRRGRR
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 PVLIPDEEEAASPHTSSNSAIICLVSELTPESEEPDQPVAPSGSSAGERPMRPR
 CSLREFARRFMALAPRDSSTSEAAGPSRLGAGPRATEPFSVAVVLVDRSSEGAGLFGG
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repeat_region 112316..112419
 /note="variable copy number in V592"
 /rpt_unit=TGCCCTAGCCCCC
 misc_feature 113013..113068
 /note="56bp insertion compared with

AB4:AATGACGTCACCGGAAGGGGAGGAGCAGGAAATGACGTAGGCGGTAGTGACGTA
 GG"

repeat_region 113045..113089
 /note="novel repeat not present in AB4"
 /rpt_unit=TGACGTAGGCGGTAG
 repeat_region 113099..113353
 /rpt_unit=GGAAGGGGAGGAGCA
 repeat_region 113358..113501
 /note="12 copies in V592 compared with 37 in AB4"
 /rpt_unit=CCATCAACCCGC
 gene 113835..148482
 /gene="EHV-1 ORF64"
 CDS complement(113835..118298)
 /note="homologous to HSV-1 RS1"
 /codon_start=1
 /product="transcriptional regulator"

/translation="MASQRSDFAPDLYDFIESNDFGEDPLIRAASAAEEGFTQPAAPD
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 QPEFPSSASPGGGSPAPRVRSISISSSSSSSSSMDEDDQADGAGASSSSSSSSSDSDS
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 AASAPAAASCAPGVYQREPLLTSPGDPWPGSDPPPMGRVRYGGTGDSRDGLWDDPEIV
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 FCQKFIHAPRGHGSFITGSVANPLPHIGDAMAAGNALWALPHAAASVAMSRRYDRTQK
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AYTRVCAALGPRRKAAAAAAPGSRAPRPSAFRLRELGDACVLACQAVFEALLRLRG
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GSDELRLAVRAVLVVARTVAPLVRYNAEGARARASAWTVTQAVFSIPSLVGGMLGEAV
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WAGNWTGAPDVSAALNAQGVLLLSTGDLAFTGCVEYLCRLGSAARRKLLVLDAVSTEDW
PQDGPASISQYHIYMRAALTFRVACAVRWPRERHLSRAVLTSSTLFGPGLFARAEAAFA
RLYPDSAPLRLCRSSNVAYTVDTRAGERTRVPLAPREYRQVRVLPDYDGCKDMRAQAE
LGFHDPDFEEGAAQSHRAANRWGLGAWLRPVYLACGRRGAGAVEPSELLIPELLSEFC
RVALLEPDAAEPLVLPITEAPRRRAPRVDPWEPGFGSRSTSVLHMGATELCLPEPDDE
repeat_region 120814..120883
                /note="10 copies in V592 compared with 16 copies in AB4"
                /rpt_unit=GGTGGTC
repeat_region 120955..121079
                /note="5 copies in V592 compared with 3 copies in AB4"
                /rpt_unit=CCCAGCTCCGGCGACCCCGGCCAG
gene          121082..141235
                /gene="EHV-1 ORF65"
CDS           121082..121963
                /gene="EHV-1 ORF65"
                /function="putative host range determinant"
                /note="homologous to HSV-1 US1"
                /codon_start=1
                /product="putative product of ORF65"

/translation="MPHGQPCGACDGSRCMAQRGTPSTSPLIPSLTPSPAGDPSPRS
SQRIDAVRVPARLPGGSDHPEYGMPLSPRALRPYLARGPGAFCAPPWRPDVNRLAGDV
NRLFRGISTSSIHVTEDSRTLRRALLDFYAMGYTHTRPTLECWQSLQLLPEQSFPRLR
ATLRALNSEDRIEQRFLPEPSDPPNTLFGEECDVSGDESPSEEEEEDEASGESSVSEF
SPEETASSEYDSFSDVGEDDSSCTGKWSSSESESDSESADPTNNHHPTTRASAAKKR
                RKRQPPKGERPTKSARR"
gene          122581..139736
                /gene="EHV-1 ORF66"
CDS           122581..123291
                /gene="EHV-1 ORF66"
                /note="homologous to HSV-1 US10"
                /codon_start=1
                /product="virion protein"

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/translation="MDGAYGHVHNGSPMAVDGEESGAGTGTGAGADGLYPTSTDAAH
 AVSLPRSVGDFAAVVRAVSAEADALRSGAGPPAEAWPRVYRMFCDMFGRYAASPMPV
 FHSADPLRRRAVGRYLVDLGAAPVETHAELSGRMLFCAYWCCLGHAFACSRPQMYERAC

ARFFETRLGIGETPPADAERYWAALLNMAGAEPELFPRHAAAAAYLRARGRKLPLQLP
 SAHRTAKTVAVTGQSINF"
 repeat_region 123549..123656
 /note="variable copy number in V592"
 /rpt_unit=AGGCCGAGCGGGGAGAGCGGTAGGGG
 gene 123853..138464
 /gene="EHV-1 ORF67"
 CDS complement(123853..124671)
 /note="virulence determinant"
 /codon_start=1
 /product="product of ORF67 (IR6)"

/translation="MNSDMMTAATAGTEVFRICALARRRNANPPHLVLAPTFAAAAAGG
 AANSSGEEAPRGERKHLFNPFGCMLGRSYFRRCREEMNEGYFAKVPTGYFPVAPSEVP
 CRVPVEGVVAGEVLSYSALPLPKIEKRFYKQLNDGTFVRLPFLYPEVYYEGEEEPAD

RYIIRADAADASSADPSTLPEEAFKVPPIAIEGITNWQGPKRIPIPSERYVMKLGFE
 YQLHVTEDAFQEVNTSEFMRLDLQSSDPHPRGARQPRSAHVFAENPEDTPVAV"
 gene complement(124839..125750)
 /gene="EHV-1 ORF68"
 CDS complement(124839..125750)
 /gene="EHV-1 ORF68"
 /function="virulence factor"
 /note="homologous to HSV-1 US2, truncated via framshift
 compared with EHV-1 strain AB4"
 /codon_start=1
 /product="virion membrane protein"

/translation="MGVVLITVTVVDRHKALPNSSIDVDGHLWEFLSRQCFVLASEP
 LGIPIVRSADLYRFSSSLTLTPKACRPVIRTRGATAIALDRNGVVYHEDRMGVSIEW
 LSVLSGYNHLNSSLIIINQPYHLWVLGAADLCKPVFDLIPGPKRMVYAEIADEFHKSWQ
 PPFVCGKLFETIPWTTVEHNNHPLKLRAAGGEDTVVGECGFSKHSSNSLVHPPTVKRVI

YAVVDPARLREIPAPGRPLPRRRPSEGGMRAPRWRSRAPAPARSTAAAATPPRPGDPR
 APAARRAGDVTWMERLLWGVFGRTSTR"
 gene 125886..127034
 /gene="EHV-1 ORF69"
 CDS 125886..127034
 /gene="EHV-1 ORF69"
 /note="homologous to HSV-1 US3"
 /codon_start=1
 /product="serine-threonine protein kinase"

/translation="MENKQCDHLTDWFSTTSDASESMDTTPPLPPPTPSVDPSYSGAA
 ADEDLYSDISEGDLEYSDCDSASESDEDDDDCLIPSKEKAREVAASFGYTVIKTLTPG
 SEGRVMVATKDGQPEPVVLKIGQKGTTLIEAMMLRNVNHPSVIQMKDTLVSGAITCMV

LPHYSSDLYFTLTKESTRIPIDQALIIEKQILEGLRYLHAQRIIHRDVKTENIFINSV
 DQVCIADFGAAQFPVVEPADLGLAGTVETNAPEVLARAKYNSKADIWSAGIVLFEMLA
 YPSTLFEDPPSTPEEYVKSCHSQLLKIISTLKINPEEFPRDPGSRLVRGYIEYSRLER
 KPYTRYPCFQRVNLHIDGEFLVHKMLAFNAAMRPSAEELLSYPMFAQL"
 gene 127156..128391
 /gene="EHV-1 ORF70"
 CDS 127156..128391
 /gene="EHV-1 ORF70"
 /note="homologous to HSV-1 US4"
 /codon_start=1
 /product="envelope glycoprotein G (gG)"
 /translation="MLTVLAALSLLSLLTSATGRLAPDELCYAEPRRTGSPNTQPER
 PPVIFEPPTIAIKAESKGCELILLDPPIDVSYRREDKVNASIAWFFDFGACRMPIAYR
 EYYGCIGNAVPSPETCDAYSFTLIRTEGIVEFTIVNMSLLFQPGIYDSGNFIYSVLLD
 YHIFTGRVTLEVEKDTNYPGMIHGLTAYGNINVDETMDNASPHPRAVGCFFPEPIDNE
 AWANVTFTTELGIPDPNSFLDDEGDYPNISDCHSWESYTPNTLRQATGPQTLLVGAVG
 LRILAQAWKFVGDETYDTIRAEAKNLETHVPSSAAESSLENQSTQEESSNSPEVAHLRS
 VNSDDSTHTGGASNGIQDCDSQLKTVYACLALIGLGTGCMIGLIVYICVLRSLKSSRN
 FSRAQNVKHRNYQRLEYVA"
 gene 128572..131172
 /gene="EHV-1 ORF71"
 CDS 128572..131172
 /gene="EHV-1 ORF71"
 /note="gp2); positional homologue of HSV-1 US5"
 /codon_start=1
 /product="envelope glycoprotein (gp300)"
 /translation="MGFIYARKLLLCMAVSIYAIGSTTTTETTTSSSSTSGSGQSTSS
 GTTNSSSSPTTSPPTTSSSPPTSTHTSSPSSTSTQSSSTAATSSSAPSTASSTTSIPT
 STSTETTTTTPTASTTTPTTTAAPTAAATTTAVTTAASTSAETTTATATATSTPTTT
 TPTSTTTTTATTTVPTTASTTTDTTTAATTTAATTTAATTTAATTTAATTTAATTTAA
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 TDTTTPSEATTATTSPSTTVSASTTSATTTAFTTESHTSPDSSTGSTSTAEPSTFT
 LTPSTATPSTDQFTGSSASTESDSTDSSTVPTTGTESITESSTTEASTNLGSSTYES
 TEALETDPGNTTSGNTTPSPSPRTPSFADTQOTPDNGVSTQHTTINDHTTANAQKHAG
 HHRGRAGGRRGSPQGGSHHTPHPDRLTPSPDDTYDDDTNHPNGRNNSIEIVPQLPPDR
 PIIELGVATLRKNFMEASCTVETNSGLAIFWKIGNASVDAFNRGTTHTRLMRNGVPVY

ALVSTLRVPWLNVIPLTKITCAACPTNLVAGDGVDLNSCTTKSTTIPCPGQQRTHIFF
 SAKGDRAVCITSELVSQPTITWSVGSDRLRNDGFSQTWYGIQPGVCGILRSEVRIHRT
 TWRFGSTSKDYLCEVSASDSKTSYKVLPNNAHSTSNFALVAATTLTVTILCLLCCLYC
 MLTRPRASVY"
 repeat_region 129121..129270
 /note="6 copies primary repeat unit, 4 copies secondary
 repeat unit: ACGACCACgGCAGCA (7 copies primary repeat
 unit
 in AB4)"
 /rpt_unit=ACGACCACAGCAGCA
 repeat_region 129328..129552
 /note="variable copy number in V592"
 /rpt_unit=ACCACCGCGGCTACC
 gene 131265..132473
 /gene="EHV-1 ORF72"
 CDS 131265..132473
 /gene="EHV-1 ORF72"
 /function="role in virus entry"
 /note="homologous to HSV-1 US6"
 /codon_start=1
 /product="envelope glycoprotein D (gD)"
 /translation="MSTFKLMDGRLVFAMAIAILSVVLSCGTCEKAKRAVRGRQDRP
 KEFPPPRYNYTILTRYNATALASPFINDQVKNDLRIVTATRPCEMIALIAKTNIDSI
 LKELAAAQKTY SARLTWFKIMPTCATPIHDVSYMKNPKLSFAMCDERSDILWQASLI
 TMAAETDDELGLVLAAPAHASAGLYRRVIEIDGRRIYTDFSVTIPSERCPIAFEQNF
 NPDRCKTPEQYSRGEVFTRRFLGEFNFPQGEHMTWLKFWFVYDGGNLPVQFYEAQAF
 RPVPPDNHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLAPRLDEVDEVIE
 PVTKPPKTSKSNSTFVGISVGLGIAGLVLVGVILYVCLRRKELKKS AQNGLTRLRST
 FKDVKYTQLP"
 gene 132581..133855
 /gene="EHV-1 ORF73"
 CDS 132581..133855
 /gene="EHV-1 ORF73"
 /function="putative Fc receptor, role in envelope
 fusion,
 interacts with gE"
 /note="homologous to HSV-1, US7"
 /codon_start=1
 /product="envelope glycoprotein I (gI)"
 /translation="MAKLTGMFSAAILLMAICSTAIIRGEHMSMYLNASSEFAVYP
 TDQSLVLVGHLLFLDGQRLPTTNYSGLIELIHNYSSVCYTVIQTISYESCPRVANNA
 FRSLHKTSKHYHDYFRVNVSVETNVLNITKPQPTDSGAYILRVKLDHAPTADVFGV
 SAFVYDLKSKTVPDPMPTTQTVEPTTSYVSTPTYDYDDVTETESTSTSTQQAMTST
 QTPSATWGTQLTTELPTNETVVGIEALLCHWFQPSTRVPTLYLHLLGRTGNLPEDVL
 LVEDSEFLRTTSPAHRPSASPADGDDFKQTNSTSLKARNKIVAMVVIPTACVLMLLLV

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VVGAIINGAVRKHLLSCASRRRIYRSGQGASAAERRRLTCGPTLAASSESLADDTTSS
      gene      PPTPKPSKKTLETDPLMEQLNRKLEAIKEES"
                134088..135740
                /gene="EHV-1 ORF74"
      CDS      134088..135740
                /gene="EHV-1 ORF74"
                /function="putative Fc receptor, role in envelope
fusion,
                interacts with gI"
                /note="homologous to HSV-1 US8"
                /codon_start=1
                /product="envelope glycoprotein E (gE)"

/translation="MELLAASRACIFFGLVTVLDAWGVQQVELSEGAWAMIDGRDVLV
PTNTTTRVTKAWTFLETPPGCAGDISVKKVCVSHSLCEDNIIIGKHCNLLTGEHGIAL
AEFNVVNGSLRRTDDVYFVNGTVFPILAETRSVLQIHRATPSIAGVYTLHVSIDGMMK
HSVVLLTVKKPPKQPQPRLRVKTPPPVTVPVKTHTDFFVHGYHSRVYADGESFEL
SVNLESHIVEPSFSAEIQWYMNNTSSSSCDLFRVFETCFIHPTAMACLHPEQHTCSFT
SPIRATKILHRVYGNCSDHGNSWPSRCHSTLLGNRLYFIQPAQNRVDLLFKDTPASAT
GLYVFFVLLYNGHPEAWTYTLLSTANHFMNVLTDVTRPRLGEHFYTDLGHKIITPHPSV
ATTEELGAWTRHYLAFLLVIICTCAALLVALVWGCILYIRSNRKPYEVLNPFETVYT
SVPSNDPSDEVLVFERLASDSDSDSDEELEYPPPKPAPQLPPYQFVDGGDAPS
      gene      GRSGFKVWFRDTPEASPVPLHKPTLQGPDYSRVASKLKSILK"
                135737..136129
                /gene="EHV-1 ORF75"
      CDS      135737..136129
                /gene="EHV-1 ORF75"
                /note="positional counterpart HSV-1 US8A"
                /codon_start=1
                /product="putative product ORF75"

/translation="MSSNSDNTECFGGVNYAEGMRKRKRNPVRNSTFQEYLDARNARY
PRSGSTSDSDEYTTTRSKYESDVSEFKKMDLETLPKPAEPQAKAEPDAAKEEPPVS
      gene      TTSYILNEWVAPMIGHFLAMCMYELLFK"
                136465..137124
                /gene="EHV-1 ORF76"
      CDS      136465..137124
                /gene="EHV-1 ORF76"
                /note="homologous to HSV-1 US9"
                /codon_start=1
                /product="tegument protein"

/translation="MEKAEAAAVVIPLSVSNPSYRSGMSDQEVSEEQSAGDAWVSAA
MAAAEAVAAAATSTGIDNTNDYTYTAASENGDPGFTLGDNITYGPNGAASGCPSPPSPE
VVGLEMVVVSSLAPEIAAAVPADTISASAAAPATRVDDGNAPLLGPGQAQDYDSESGC
YYSESNETASMFIRRVGRRQARRHRRRRVALTVAGVILVVVLCAISGIVGAFLARVF
      P"
      CDS      137646..138464

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found      /gene="EHV-1 ORF67"
           /note="virulence determinant, identical sequence as

           in span 124671-123853"
           /codon_start=1
           /product="product of ORF67 (IR6)"

/translation="MNSDMMTAATAGTEVFRICALARRRRNANPPHLVLAPTFAAAAAGG
AANSSGEEAPRGERKHLFNPFGCMLGRSYFRRCREEMNEGYFAKVPTGYFPVAPSEVP
CRVPVEGVVAGEVLSYSALPLPKIEKRFYKQLNDGTFVRLPFLYPEVYYEGEEEPAD
E
RYYIRADAADASSADPSTLPEEAFKVPPIAIEGITNWQGPRIPIPSERYVMKLGFE
      YQLHVTEDAFQEVNTSFMRLDLQSSPDHPHPRGARQPRSAHVFAENPEDTPVAV"
      repeat_region 138661..138768
                    /note="variable copy number in V592, identical
                    complementary sequence to span 123549-123656"
                    /rpt_unit=CCCCTACCGCTCTCCCCCGCTCGGCCCT
      CDS            complement(139026..139736)
                    /note="homologous to HSV-1 US10, identical sequence as
                    found in span 122581-123291"
                    /codon_start=1
                    /product="virion protein"

/translation="MDGAYGHVHNGSPMAVDGEESGAGTGTGAGADGLYPTSTDAAH
AVSLPRSVGDFAAVVRVSAEAADALRSGAGPPAEAWPRVYRMFCDMFGRYAASPMPV
FHSADPLRRAVGRYLVDLGAAPVETHAELSGRMLFCAYWCCLGHAFACSRPQMYERAC
ARFFETRLGIGETPPADAERYWAALLNMAGAEPPELFRHAAAAAYLRARGRKLPLQLP
      SAHRTAKTVAVTGQSINF"
      CDS            complement(140354..141235)
                    /function="putative host range determinant"
                    /note="homologous to HSV-1 US1, identical sequence as
                    found in span 121082-121963"
                    /codon_start=1
                    /product="putative product of ORF65"

/translation="MPHQPCGACDGSRCMAQRGTPSTSPLIPSLTPSPAGDPSPRS
SQRIDAVRVPARLPGGSDHPEYGMPLSPRALRPYLARGPGAFCAPPWRPDVNRLAGDV
NRLFRGISTSSIHVTEDSRTLRRALLDFYAMGYTHTRPTLECWQSLQLLPEQSFPLR
ATLRALNSEDRYEQRFLPEPSPDPNTLFGEECDVSGDESPSEEEEEDEASGESSVSEF
SPEEETASSEYDSFSDVGEDDSSCTGKWSSSESESDSESDAPTNNHHPTTRASAACKR
      RKRQPPKGERPTKSARR"
      repeat_region 141238..141362
                    /note="5 copies in V592 compared with 3 copies in AB4,
                    identical complementary sequence to span 120955-121079"
                    /rpt_unit=CTGGGCCGGGGTCGCCGGAGCTGGG
      repeat_region 141434..141503
                    /note="10 copies in V592 compared with 16 copies in AB4,
                    identical complementary sequence to span 120814-120883"
                    /rpt_unit=gaccacc
      CDS            144019..148482
                    /gene="EHV-1 ORF64"
                    /note="homologous to HSV-1 RS1, identical sequence as

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found in span 118298-113835"
 /codon_start=1
 /product="transcriptional regulator"

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/translation="MASQRSDFAFDLYDFIESNDFGEDPLIRAASAAEEGFTQPAAPD
LLYGSQNMFGVDDAPLSTPAVVIPPPSPAPEPRGGKAKRSPSAAGSGGPPTAAAAQP
ASPAPSPAPGLAAMLKMHSSVAPGNRRATGSSSPGGGDAADPVALDSDTETCPGSP
QPEFPSSASPGGGSPAPRVRSISISSSSSSSSSMDEDDQADGAGASSSSSSSSDDSDS
DEGGEEETPRPRHSQNAAKTPSAAGSPGPSSGGDRPAAGAATPKSCRGAASPGAPAP
APASAPAPSRPGGGLLPPGARILEYLEGVREANLAKTLERPEPPAGMASPPGRSPHRL
PKDQRPKSALAGASKRKRRANPRPIPQTQTQAPAEAPQTAVWDLDMNSSQATGAAAA
AASAPAAASCAPGVYQREPLLTSGDPWPWGSDPPPMGRVRYGGTGDSRDGLWDDPEIV
LAASRYAEAQAPVPVFPVPEMGDSTKQYNALVRMVFESEAMSRLQNSKLSGQDQNLAQ
FCQKFIHAPRGHSFITGSVANPLPHIGDAMAAGNALWALPHAASVAMSRRYDRTQK
SFILQSLRRAYADMAYPRDEAGRPDSLAAVAGYPAQAAAAAASQQQPEAPAPSVRVRE
AYTRVCAALGPRRKAAAAAAGPSRAPRPSAFRLRELGDACVLACQAVFEALLRLRGG
ASAVPGLDPSEIPSPACPPEALCSNPAGLETAALSLEYELDLVERARLLGDSDPHRL
GSDELRLAVRAVLVVARTVAPLVRYNAEGARARASAWTVTQAVFSIPSLVGGMLGEAV
SLLAPPTRSQQPSSSSPGGEPFSGSAAEGSLQTLPLWPTVPGKQSATVPSSHQSQP
QHSQSGGGAGATTATCCRATQTNARSRGQHQPKARSPQAAASPAHLSQEAMPGSSS
DDRAIHGRPRGKSGKRRSEPLEPAAQAGASASFSSSARGYDPSGPVDSPPAPKRRVAT
PGHQAPRALGMPAEGPDRRGFRVRPRGDCHTPRPSDAACAAYCPPELVAELIDNQL
FPEAWRPALTFDPQALATIAARCSGPPARDGARFGELAASGPLRRRAAWMHQIPDPED
VKVVVLYSPLQDEDLGGLPASRPGGSRRPLWSDLKGGLSALLAALGNRILTKRSHA
WAGNWTGAPDVSAALNAQGVLLSTGDLAFTGCVEYLCRLGSARRKLLVLDAVSTEDW
PQDGPASISQYHIYMRAALTFRVACAVRWPRERHLSRAVLTSSTLFGPGLFARAEAAFA
RLYPDSAPLRLCRSSNVAYTVDRAGERTRVPLAPREYRQRVLPDYDGCKDMRAQAEG
LGFHDPDFEEGAAQSHRAANRWGLGAWLRPVYLACGRRGAGAVEPSELLIPELLSEFC
RVALLEPDAAEAPLVLPITEAPRRRAPRVDWEPPGFSRSTSVLHMGATELCLPEPDDE
    repeat_region  LEIDGAGDVELVVEHPGPSQVAQALRRAPIKIEVVSDDDEDGGDWCNPYLS"
    identical      148816..148959
                   /note="12 copies in V592 compared with 37 in AB4,
                   complementary sequence to span 113358-113501"
    repeat_region  /rpt_unit=GCGGGTTGATGG
                   148964..149218
                   /note="identical complementary sequence to span

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113099-113353"
/rpt_unit=TGCTCCTCCCCTTCC
repeat_region 149228..149272
/note="novel repeat not present in AB4, identical
complementary sequence to span 113045-113089"
/rpt_unit=CTACCGCCTACGTCA
misc_feature 149249..149304
/note="56bp insertion compared with

AB4:CCTACGTCACTACCGCCTACGTCATTTCTGCTCCTCCCCTTCCGGTGACGTCA
TT, identical complementary sequence to span
113013-113068"
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SEQUENCE ANNEX 2 - PCR amplification and sequencing primers

Gene	AMPLIFICATION		SEQUENCING	
	Name	Sequence	Name	Sequence
ORF 8	ORF8f	AATTATTGGTGGGCAGAACC	ORF8s	CCATCACCACGCTATTCTC
	ORF8r	TTCTCCAGCACAGCAACG		
ORF11	ORF11f	CTGTAACGATGCTAACGCTACG	ORF11sf1	TAGCCCAAACGACGACAAAG
	ORF11r	TTCAGAAACCTGTCCAGGTCC		
ORF14	ORF14f	CCCCAACTCTAAAACTCG	ORF14s	TTTACACCAATCCACTCC
	ORF14r	AATGTACCATAACACAACCTCC		
ORF15	ORF15f	CAAAGCGCAAAGCAAAATGC	ORF15sf1	ATCCAACACACGCAACATC
	ORF15r	GGGCCTTGATAGTCAGCTCTCC		
ORF30	ORF30f	GCGCTACTTCTGAAAACG	ORF30s	TACCCAAGCATTATCCAG
	ORF30r	CCACAACTTGATAAACACG		
	ORF30f2	AAACCACAAGCCTTACTCC	ORF30s2	GAGAAGACCTTTCAGCGAC
	ORF30r2	GCGCAACTATCACATACG		
ORF33	ORF33f1	TCAAGGAGGAACTAGCTCG	ORF33s1	GTATTCTCCTCGGTTTTTC
	ORF33r1	CCAAAAAGCAACAAACAGG		
	ORF33f2	TTTACGACATCGACAGC	ORF33s2	ACAAAGCCAAAACCTTCCTAC
	ORF33r2	GAGGTCACACTTTGAGTACG		
ORF34	ORF34f	ATTCTCCACGCGGTATCTCC	ORF34s	CGATGTAGACGGACCAGAAG
	ORF34r	ATGTCAAGCGCCATAGAAACG		
ORF37	ORF37f	ACATACTCCGCCATCTCC	ORF37s	CCATCTATAACGCCAGCC
	ORF37r	ACAGCTACATGACTCGTGC		
ORF39	ORF39f	TTACGTACTCAGCGATGG	ORF39s	TAAGAGCACGGATGTAAG
	ORF39r	GGGATAGAAATAGCGAGG		
ORF40	ORF40f	ATCACAAACGCATCCTCG	ORF40s	ACTCGCCGAATCCCAGATG
	ORF40r	CACAGCTCACCCAAAATACC		
ORF52	ORF52f	CCAACAGCTTTCACATCACC	ORF52s	GCTACTTCGTTCACTTCC
	ORF52r	TTCAAATTCTCGCTCACC		
ORF67	ORF67f	CAAAACTCCAACACCACG	ORF67s	GAAGAAGCATTCGCCAAG
	ORF67r	GAGAAGAGGTTCTACAAGCAGC		
ORF68	ORF68f	AGCATTGCCAAACAGTTCC	ORF68s1	GAAGATAGAATGGGTGTGAG
	ORF68r	CAAGAAACCACTGCTCAACC	ORF68s2	AAACCACTGCTCAACCCAC
			ORF68s3	ACCGTTGAGCATAATCATCC
ORF73	ORF73f	GAACATATGAGCATGTACC	ORF73s	ACGGACAACGCTTACCCAC
	ORF73r	GACCAGTAGAACATCTTCC		

SEQUENCE ANNEX 3a -DNA sequence of EHV-1 (strain V592) ORF30

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1   ATGGCGGCGC GCGAACAGGC CAACTCCGTT CGCAGGAGCG GGTTTTTTTAA
51  TCCGTTTATT GGCAAGAGGC CATTTTTTCAG GCCGGGAAGC GGGCAGACCG
101 CGGAGACAGA GCGCCCAAGG CCCCCCAAC ACTCGTACTG CACAGAGGTG
151 GGTAGCTTTA AGTTTATAGC TCCAAGATGC CTCGATGAAG AAGCCCCCGC
201 CGACCAGCGA CGCGGTGTAC ACGTGGGCAC CTTGGAGCGC CCACCCAAAG
251 TGTACTGCGA TGGCTCAGAG TACGACGTGC TGAACTTTGC CTCCGGAGGT
301 TGCTGGCCTC GCAGGATTCG GGTTTGGAAC GGCCAGGATT TTCGGGGCGA
351 TGGATTCAAC CCCAGATTTG AGAGATTTCA CGTGACGAC ATAGTAGAGA
401 CTTCCGAGAG GCCTCACAC GATGACCCAT CCAGGTTTGC TGAGCTATCC
451 CGCCCAAGCG GGTCTGTGGT AACACTGCTG GGAATGAGCG AGTGTGGAAG
501 GCGAGTCGCG GTTACAGTCT ATGGTGTGCG CCATTATTTT TACATGGCAA
551 AGGCGGAGGT GGATAGCGCT TGTGGAATAA CCACCGAGGC AGAATCTGTG
601 CGCGCAATGG TGGACTGCGC GCACAGCTCG GCTTTGAGCG CGGCCCTGGG
651 AAATGGCAAC GGCGGCAAAAC AGAGCGGCGG CAGCGGCGGG GGATGGTGGG
701 GCGGAAAGCA CGTGTCTGCG GACTGCTTCA AAGTGGAGAC CGTGTGCCAC
751 ACGACGCTGT ACTACTTTGG ATCTAAGCCA GCTCTCTACT ATAGAGTATC
801 TGCCTCCAGC AGCCGCCTGG GAGGGTTCAT CTGCGACAAC TTTCACCCGG
851 AGATTACAAA ATTCGAGGGG AGCGTGGACG TGACCACGCG GCTGTGTGTG
901 GACAATGAAA ATTTTACCAG TTTTGGGTGG TACCGCCTGC GACCCGGCAC
951 CCACGGAGAG CGTGTTCAAC TTCGCCCCGT TGAGCGACAC GTCACCTCAA
1001 GCGACGTGGA GATTAAGTGT ACTCCGATA ACCTGGAGCC GATACCAGAC
1051 GAGGCTGCCT GGCCCGACTA TAAGCTCATG TGCTTTGATA TAGAGTGTA
1101 AGCTGGAACG GGTAACGAAA TGGCGTTCCC AGTGGCAACT AACCAAGAGG
1151 ACCTGGTCAT CCAGATCTCC TGTCTGCTGT ACTCGCTTGC TACTCAGAAC
1201 CACGAACACA CCCTGCTGTT TTCCCTCGGG TCATGCGATA TCTCTGAGGA
1251 ATACTCGTTT GCATGCGTCC AGCGCGGCGA GCCAGACCG ACGGTTTTGG
1301 AGTTTGACAG CGAGTACGAG CTGCTGGTTG CTTTCTGAC CTTTCTCAAG
1351 CAGTACTCTC CCGAGTTGCG CACCGGCTAC AACATCGTTA ATTTTGACTG
1401 GGCGTACATA GTTAACAAGG TAACGTCGGT GTATAACATC AAGCTGGACG
1451 GGTACGGCAA GTTCAACAAA GGGGGGCTGT TTAAGGTGTG GGACATCGCC
1501 ACGAACCATT TTCAGAAGAA GAGCAAGGTG AAAATCAATG GCCTGATATC
1551 TCTAGACATG TATTCTGTGG CGACGGAAAA GCTAAAGCTA CCCAGCTACA
1601 AACTCGACGC GGTCTGTTGG GAGTCTCTCG GCGAGCATAA GATAGACCTT
1651 CCCTATAAAG AAATACCCTC CTATTACGCG GGAGGGCTG ACCGGAGGGG
1701 CGTAATAGGA GAGTATTGTA TCCAGGACTC TAGGCTGGTG GGCAAGCTGT
1751 TTTTTAAGTA CCTCCCCCAT CTGGAAGTAT CGGCGGTGGC CAAACTCGCC
1801 CGTATCACCC TAACGCGGGT AATTTTTGAC GGTACAGCAA TTCGCGTGTA
1851 CACGTGCTTG CTGAAACTCG CCCGCGAGAG AAATTTTATT TTGCCAGACA
1901 ACAGACGCCG GTTTGACAGT CAGGCAGACG CCGCGTCAGA GACTTCGGAG
1951 TTGGCTATGG ATAGCCAAAG CCACGCCTTC GACAGTACAG ACGAACCCGA
2001 CGGTGTGGAC GGTACCCCGG AGCCCGCAGG ATCTGGCGCT ACTTCTGAAA
2051 ACGGAGGCGG GAAGCCCGGC GTCGGGAGGG CCGTGGGCTA CCAGGGAGCA
2101 AAGGTTCTAG ACCCCGTATC CGGCTTTTAT GTGGACCCCG TGGTTGTGTT
2151 TGACTTCGCT AGCTTATACC CAAGCATTAT CCAGGCCCAT AACCTCTGTT
2201 TCACCACCTT GCGCTCGAT GAAGTGGATC TGGCCGGGCT TCAACCATCC
2251 GTCAACTACT CGACGTTTCA GGTGGGTGAC CAAAAGTTAT TTTTGTCCA
2301 CGCCCATATT CGCGAAAGCC TGCTTGGCAT CTTGCTGCGC GACTGGCTGG
2351 CCATGCGAAA GGCGGTGAGG GCGCGAATCC CCACCAGCAC CCCCAGGAG
2401 GCAGTTTTAC TAGATAAGCA GCAGTCTGCG ATTAAGGTGA TATGCAACTC
2451 GGTTTACGGA TTCACGGGGG TGGCAAACGG CCGTTTGCCG TGTCTGAGGA
2501 TAGCGGCTAC CGTTACCACG ATAGGACGCG ACATGCTCCT CAAGACCCGA
2551 GATTACGTTT ACTCTCGTTG GGCGACGCGC GAGCTGCTGG AGGACAATTT
2601 TCCAGGGGCT ATAGGTTTCC GAAACCACAA GCCTTACTCC GTCAGGGTTA
2651 TCTACGGAGA CACCGACTCC GTGTTTATCA AGTTTGTGGG CCTGACGTAC
2701 GAGGGGGTAT CGGAGCTGGG GGATGCTATG TCGCGTCAGA TTTCAGCGGA
2751 CCTCTTTAGA GCGCCCATCA AACTGGAGTG TGAGAAGACC TTTCAGCGAC
2801 TGCTGCTGAT CACCAAGAAG AAGTACATAG GTGTCATAAA CGGGGGGAAG
2851 ATGCTCATGA AGGGGGTCGA CCTGGTCCGC AAAAATAACT GCTCTTTCAT
2901 AAATTGTGAC GCGCGACATC TGGTAGATCT TTTGTTGTAC GACGAGGATG

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2951 TGGCCACGGC GGCAGCAAAG GTGACAGACG TGCCTCCCGC AGAATGGGTG
3001 GGGCGCCCGC TACCGAGCGG CTTTGACAAG TTTGGGCGAG TGCTGGTAGA
3051 GGCGTACAAC CGTATCACTG CCCCCAACTT GGACGTGCGC GAGTTCGTTA
3101 TGA CTGCTGA GCTGAGCCGC TCACCCGAAT CGTATACCAA CAAGCGCCTG
3151 CCGCACCTCA CCGTCTACTT TAAGCTCGCC ATGAGGAATG AAGAACTGCC
3201 CAGCGTAAAA GAGAGAATTC CGTATGTGAT AGTTGCGCAG ACCGAGGCCG
3251 CGGAACGCGA AGCGGGTGTA GTAAACTCAA TGC GCGGTAC CGCCCAAAC
3301 CCCGTGGTAA CCAAGACCGC ACGCCCCCAA CCTAAACGCA AACTGCTGGT
3351 TTCCGACCTC GCCGAAGACC CGACCTATGT TTCCGAGAAT GACGTACCGC
3401 TAAACACAGA CTACTATTTT TCCCACCTGT TGGGTACCAT AAGCGTGACC
3451 TTTAAGGCTC TATTCGGAAA TGATGTGAGA ACAACAGAAA ATCTTTTAAA
3501 GCGGTTTATT CCGGAAACCC CCCACAAGAC CCCCACGAAA ACCCAGGCAC
3551 TGCTTGAGCG CGCCGGCTTT GAAAAGCTGA CGCCCTTTAC ACCGGAGGAA
3601 GAAAGTCGTC GAATACTGCA TACAGTTTTT TGTACTCTAG AAGCAGCTCC
3651 CCATCAAAGC TGA

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SEQUENCE ANNEX 3b - Amino acid sequence of EHV-1 (strain V592) ORF30

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1   MAAREQANSV RRSGFNPF I GKRPFFRPGS GQTAETERPR PPQHSYCTEV
51  GSFKFIAPRC LDEEAPADQR RGVHVGTLER PPKVYCDGSE YDVLNFASGG
101 CWPRRIRVWN GQDFRGDGFN PRFERFHVYD IVETSESASH DDPSRFAELS
151 RPSGSVVTLL GMSECGKRVA VHVGVRHYF YMAKAEVDSA CGITTEAELV
201 RAMVDCAHSS ALSAALGNNG GKGQSGGSGG GWWGGKHVSA DCFKVETVCH
251 TTLYYFGSKP ALYYRVSASS SRLGGFICDN FHPEITKFEG SVDVTTRLLL
301 DNENFTSFGW YRLRPGTHGE RVQLRPVERH VTSSDVEINC TPDNLEPIPD
351 EAAWPDYKLM CDFIECKAGT GNEMAFPVAT NQEDLVIQIS CLLYSLATQN
401 HEHTLLFSLG SCDISEEYSF ACVQRGEPRP TVLEFDSEYE LLVAFITFLK
451 QYSPEFATGY NIVNFDWAYI VNKVTSVYNI KLDGYGKFNK GGLFKVWDIA
501 TNHFQKKSKV KINGLISLDM YSVATEKLKL PSYKLDVAVG DVLGEHKIDL
551 PYKEIPSYYA GGPDRRGVIG EYCIQDSRLV GKLEFFKYLPH LELSAVAKLA
601 RITLTRVIFD GQQIRVYTCL LKLARERNFI LPDNRRRFD$ QADAASETSE
651 LAMDSQSHAF DSTDEPDGVD GTPDAAGSGA TSENGGGKPG VGRAVGYQGA
701 KVLDPVSGFH VDPVVVFDFA SLYPSIIQAH NLCFTTLALD EVDLAGLQPS
751 VNYSTFEVGD QKLFFVHAHI RESLLGILLR DWLAMRKAVR ARIPTSTPEE
801 AVLLDKQOSA IKVICNSVYG FTGVANGLLP CLRIAATVTT IGRDMLLKTR
851 DYVHSRWATR ELLEDNFPGA IGFRNHKPYS VRVIYGD TDS VFIK FVGLTY
901 EGVSELGDAM SRQISADLFR APIKLECEKT FQRLLLITKK KYIGVINGGK
951 MLMKGVDLVR KNNCSFINLY ARHLVDLLLY DEDVATAAAK VTDVPPAEWV
1001 GRPLPSGFDK FGRVLVEAYN RITAPNLDVR EFVMTAELSR SPESYTNKRL
1051 PHLTVYFKLA MRNEELPSVK ERIPYVIVAO TEAAEREAGV VNSMRGTAQN
1101 PVVTKTARPO PKRKLLVSDL AEDPTYVSEN DVPLNTDYYF SHLLGTISVT
1151 FKALFGNDVR TTENLLKRFI PETPHKTPTK TQALLERAGF EKLTPFTPEE
1201 ESRRILHTVF CTLEAAPHQS

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Figure 1. Multi-locus sequence analysis

Outbreak	ORF marker region																Disease
	68	8	11	14	15	30-m1	30-m2	33-m1	33-m2	34	37	39	40	52	67	73	
GB83/1/1	1	1	1	1	1	2	1	1	1	1	1A	1	1	1	1*	1	Non-paralytic
GB83/3/1	1	1	-	1B	-	2	1	1	1	1	1A	1	1	1	1*	-	
GB86/1/1	1	1	1	2	1	2	1	1	1	1	1A	2	1	1	1*	1	
US85/1/1	1A	-	1	1	1	2	1	1	1	1	-	1	1	1	1	1	
GB80/1/2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	Paralytic
GB93/4/2	1*	1	1	1	1	1	1	1	1	1	1A	1	1	1	1*	-	
GB81/4/1	2A	1	1	1	1	2	1	1	1	1	1A	1	1	1	1*	-	Non-paralytic
GB86/2/1	2	1	-	1	-	2	1	1	1	1	1A	1	1	1	1*	-	
US76/1/1	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US79/1/1	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US83/1/1	2	-	-	1	-	2	1	1	1	1	-	-	-	-	-	-	Paralytic
US83/2/1	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US84/1/1	2	-	-	2	-	2	1	1	1	1	-	-	-	-	-	-	
US99/1/1	2	-	1	2	2	2	1	2	2	2A	2	2	1	-	1	1	
US00/1/1	2	-	-	2	-	2	1	1	1	1	-	-	-	-	-	-	Paralytic
GB93/5/2	2*	1	-	-	-	-	-	-	-	-	1A	-	-	-	-	-	
GB99/1/2	2	-	1	-	2	1	-	-	2	-	-	2	-	-	-	-	
GB02/2/2	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	
GB03/2/2	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	Non-paralytic
US70/1/2	2	-	1	1A	1	1	1	1	2	1	1A	1	1	1	-	1	
US85/2/2	2	-	1	2	-	2	1	1	1	1	1A	1	1	1	1	1	
US86/2/2	2	-	-	2	-	1	-	1	1	1	-	-	-	-	-	-	
US86/3/2	2	-	1	2	1	1	1	1	1	1	-	-	-	-	-	-	Non-paralytic
GB81/1/1	3	-	1	1	-	2	1	1	1	1	1A	2	1	1	1	1	
GB83/2/1	3*	1	-	2A	-	2	-	2	2	1*	2	2	1	2	1*	-	
GB85/2/1	3*	1	-	-	-	-	1	2	2	1*	2	2	-	-	-	1*	
GB88/1/1	3*	1	-	2A	-	2	1	2	2	1	2	2	1	2	-	-	Paralytic
GB89/1/1	3A	1	1	2A	2	2	1	2	2	1	2	2	1	2	1*	1	
GB89/2/1	3A	1	-	2A	-	2	-	2	2	1*	2	2	1	2	1*	-	
GB89/3/1	3*	1	-	2A	-	2	1	2	2	1*	2	2	1	2	1*	-	
GB91/2/1	3	1	-	-	-	2	1	2	2	1	2	2	1	2	1*	-	Non-paralytic
GB93/1/1	3*	-	-	-	-	2	1	-	-	-	-	2	-	-	-	-	
GB93/2/1	3*	1	-	2A	-	2	1	2	2	-	2	2	1	2	1*	-	
GB93/3/1	3*	1	-	2A	-	2	1	2	2	1*	2	2	1	2	1*	-	
GB00/2/1	3	-	-	-	-	2	-	-	2	-	-	2	-	2	-	-	Paralytic
GB01/1/1	3	-	-	2A	-	2	1	2	2	-	-	2	1	2	1*	-	
GB02/1/1	3	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
US86/1/1	3	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	
GB88/2/2	3	1	1	2	2	1	1	2	2	1	2	2	1	2	1	1	Non-paralytic
GB03/3/2	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	
GB03/4/2	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	
GB81/2/1	4	1	1	2A	2	2	1	2	2	1	2	2	1	2	1	-	
GB81/3/1	4	-	1	2A	2	2	1	2	2	1/2*	2	2	1	2	1*	1	Paralytic
GB00/1/1	4A	-	1	2A	2	2	1	2	2	1/2*	2	2	1	2	1	-	
GB80/2/2	4*	-	-	-	-	1	1	2	2	1	-	2	-	-	-	-	
GB86/3/2	4B	1	1	-	2	2	1	2	2	1	2	2	1	2	1	-	
US86/4/2	4	-	1	2A	2	1	1	2	2	2B	2	2	1	2	1*	1	Attenuated
PL68/1/0	5	1	-	3	-	1A	-	-	-	1	2	-	-	-	-	-	
US72/1/0	5	-	-	2*	-	1	-	2	2	2	-	-	-	-	-	-	
US75/1/1	5	-	1	2*	2	2	1	2	2	2A	2	2	1	2	-	1	
US81/1/1	5	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	Non-paralytic
US41/1/2	5	1	-	2B	-	1	-	-	-	2	2	-	-	-	-	-	
US79/2/2	5	-	-	-	2	1	1	2	2	2A	-	-	-	-	-	-	
US82/1/2	5	-	-	2*	-	1	1	2	2	2B	-	-	-	-	-	-	
US83/3/2	5	-	-	2*	-	1	1	2	2	2	-	-	-	-	-	-	Paralytic
US99/2/2	5	-	1	2*	2	1	1	2	1	1	2	2	1	2	1A	1	
US99/3/2	5	-	1	2*	2	2B	1	2	2	2A	2	2	1	2	1A	1	
US01/1/2	5	-	-	-	-	1	1	2	2	2	-	-	-	-	-	-	
US02/1/2	5	-	1	2	-	2B	1	2	2	1/2*	2	2	1	2	1A	1	Non-paralytic
GB85/1/1	6	2	2	2	2	2	2	2	2	3	2	3	2	2	2	2	
GB91/1/1	6*	2	2	2A	2	2	2	2	2	3	2	3	2	2	2*	2	
GB00/3/1	6*	-	-	2	-	2A	2	2	2	-	-	3	2	2	2*	-	
GB01/2/1	6	-	2	2	2	2A	2	2	2	3*	2	3	2	2	2*	2	